

[illegible]

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<130> DX0903K1

<141>

<170> PatentIn Ver. 2.0

<211> 468

<212> DNA

<213> primate

 $\langle 220 \rangle$

<221> misc feature

 $\langle 222 \rangle$ (301)

<223> nucleotide may be A, C, G, or T

 $\langle 220 \rangle$

<221> CDS

<222> (20) .. (466)

<220>

<221> mat peptide

 $\langle 222 \rangle \quad (11\bar{9}) \dots (466)$ $\langle 400 \rangle$ 1

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gta ggg ctg gtg tta act tac gac ttc act aac tgt gac ttt gag aag	148
Val Gly Leu Val Leu Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys	
-5 -1 1 5 10	
att aaa gca gcc tat ctc agt act att tct aaa gac ctg att aca tat	196
Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr	
15 20 25	
atg agt ggg acc aaa agt acc gag ttc aac aac acc gtc tct tgt agc	244
Met Ser Gly Thr Lys Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser	
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aat cgg cca cat tgc ctt act gaa atc cag agc cta acc ttc aat ccc	292
Asn Arg Pro His Cys Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro	
45 50 55	
aac cgc cgn gtg cgg tcg ctc gcc aaa gaa atg ttc gcc atg aaa act	340
Asn Arg Xaa Val Arg Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr	
60 65 70	
aag gct gcc tta gct atc tgg tgc cca ggc tat tcg gaa act cag ata	388
Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile	
75 80 85 90	
aat gct act cag gca atg aag aag agg aga aaa agg aaa gtc aca acc	436
Asn Ala Thr Gln Ala Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr	
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Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala
65 70 75

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5 10 15 20

aaa gac ctg att aca tat atg agt ggg acc aaa agt acc gag ttc aac 192
Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser Thr Glu Phe Asn
25 30 35

aac acc gtc tct tgt agc aat cgg cca cat tgc ctt act gaa atc cag 240
Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu Thr Glu Ile Gln
40 45 50

agc cta acc ttc aat ccc acc gcc ggc tgc gcg tcg ctc gcc aaa gaa 288
Ser Leu Thr Phe Asn Pro Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu
55 60 65

atg ttc gcc atg aaa act aag gct gcc tta gct atc tgg tgc cca ggc 336
Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly
70 75 80

tat tcg gaa act cag ata aat gct act cag gca atg aag aag agg aga 384
Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala Met Lys Lys Arg Arg
85 90 95 100

TC03260" 4779660

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caa gga ttg tgg cgt cgc ttc aat cga cct tta ctg aaa caa cag taa 480
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Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser Thr Glu Phe Asn
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Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu Thr Glu Ile Gln
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Ser Leu Thr Phe Asn Pro Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu
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Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly
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Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala Met Lys Lys Arg Arg
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Trasac "ChE660"

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 Phe Phe Lys Lys His Ser Cys Asp Asp Asn Lys Glu Ala Ser Phe Leu
 65 70 75 80
 Asn Arg Ala Ala Arg Lys Leu Lys Gln Phe Leu Lys Met Asn Ile Ser
 85 90 95
 Asp Asp Phe Lys Leu His Leu Ser Thr Val Ser Gln Gly Thr Leu Thr
 100 105 110
 Leu Leu Asn Cys Thr Ser Lys Gly Lys Gly Arg Lys Pro Pro Ser Leu
 115 120 125
 Gly Glu Ala Gln Pro Thr Lys Asn Leu Glu Glu Asn Lys Ser Leu Lys
 130 135 140
 Glu Gln Arg Lys Gln Asn Asp Leu Cys Phe Leu Lys Ile Leu Leu Gln
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 Phe Phe Lys Lys His Ser Cys Asp Asp Asn Lys Glu Ala Ser Phe Leu
 65 70 75 80
 Asn Arg Ala Ser Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ile Ser
 85 90 95
 Asp Asp Phe Lys Leu His Leu Ser Thr Val Ser Gln Gly Thr Leu Thr
 100 105 110

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Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
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Glu Gly Lys Ala Tyr Glu Ser Val Leu Met Ile Ser Ile Asp Glu Leu
35 40 45

Phe Phe Arg Lys His Val Cys Asp Asp Thr Lys Glu Ala Ala Phe Leu
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Asn Arg Ala Ala Arg Lys Leu Lys Gln Phe Leu Lys Met Asn Ile Ser
85 90 95

Glu Glu Phe Asn Val His Leu Leu Thr Val Ser Gln Gly Thr Gln Thr
100 105 110

Leu Val Asn Cys Thr Ser Lys Glu Glu Lys Asn Val Lys Glu Gln Lys
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Cys Trp Asn Lys Ile Leu Lys Gly Ser Ile
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35 40 45

Asp Lys Met Thr Gly Thr Asp Ser Asp Cys Pro Asn Asn Glu Pro Asn
50 55 60

Phe	Phe	Lys	Lys	His	Leu	Cys	Asp	Asp	Thr	Lys	Glu	Ala	Ala	Phe	Leu
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Asn	Arg	Ala	Ala	Arg	Lys	Leu	Arg	Gln	Phe	Leu	Lys	Met	Asn	Ile	Ser
				85					90					95	
Glu	Glu	Phe	Asn	Asp	His	Leu	Leu	Arg	Val	Ser	Asp	Gly	Thr	Gln	Thr
			100					105					110		
Leu	Val	Asn	Cys	Thr	Ser	Lys	Glu	Glu	Lys	Thr	Ile	Lys	Glu	Gln	Lys
		115					120					125			
Lys	Asn	Asp	Pro	Cys	Phe	Leu	Lys	Arg	Leu	Leu	Arg	Glu	Ile	Lys	Thr
	130					135					140				
Cys	Trp	Asn	Lys	Ile	Leu	Lys	Gly	Ser	Ile						
145					150										

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